

Conseiller.ST25  
SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel  
Debussche, Laurent  
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-1(p53)

<400> 1

agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' -393 (p53)

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<400> 2  
agatctcatc agtctgagtc aggcccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide H175 3'

<400> 3  
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15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide w248 3'

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15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide H273 3'

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15

<210> 6

<211> 15

<212> DNA

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<213> Artificial Sequence

<220>  
<223> oligonucleotide G281 3'

<400> 6  
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15

<210> 7

<211> 23

<212> DNA

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23

<210> 8

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<213> Artificial Sequence

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<223> Murine MBP1 C-term fragment

<220>  
<221> CDS  
<222> (1)..(885)

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ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg 96  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct 144  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca 192  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt 240  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
3

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65				70				75				80					
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gat Asp	gag Glu	tgc Cys	ggc Gly 100	tac Tyr	tcc Ser	agt Ser	tac Tyr	ctc Leu 105	tgc Cys	cag Gln	tac Tyr	cgc Arg	tgt Cys 110	gtc Val	aac Asn	336	
gag Glu	cca Pro	ggc Gly 115	cga Arg	ttc Phe	tcc Ser	tgt Cys	cac His 120	tgc Cys	cca Pro	caa Gln	ggc Gly	tac Tyr 125	cag Gln	ctg Leu	ctg Leu	384	
gct Ala	aca Thr 130	agg Arg	ctc Leu	tgc Cys	caa Gln	gat Asp 135	att Ile	gac Asp	gag Glu	tgt Cys	gaa Glu 140	aca Thr	ggg Gly	ggt Gly	gca Ala	cac His	432
caa Gln 145	tgt Cys	tct Ser	gag Glu	gcc Ala	caa Gln 150	acc Thr	tgt Cys	gtc Val	aac Asn	ttc Phe 155	cat His	ggg Gly	ggg Gly	tac Tyr	cgc Arg 160	480	
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aac Asn	cgc Arg	tgc Cys	ctc Leu 180	tgc Cys	cct Pro	gcc Ala	tcc Ser	aat Asn 185	ccc Pro	ctt Leu	tgt Cys	cga Arg	gag Glu 190	cag Gln	cct Pro	576	
tca Ser	tcc Ser	att Ile 195	gtg Val	cac His	cgc Arg	tac Tyr	atg Met 200	agc Ser	atc Ile	acc Thr	tca Ser	gag Glu 205	cga Arg	agt Ser	gtg Val	624	
cct Pro	gct Ala 210	gac Asp	gtg Val	ttt Phe	cag Gln	atc Ile 215	cag Gln	gca Ala	acc Thr	tct Ser	gtc Val 220	tac Tyr	cct Pro	ggg Gly	gcc Ala	672	
tac Tyr 225	aat Asn	gcc Ala	ttt Phe	cag Gln	atc Ile 230	cgt Arg	tct Ser	gga Gly	aac Asn	aca Thr 235	cag Gln	ggg Gly	gac Asp	ttc Phe	tac Tyr 240	720	
att Ile	agg Arg	caa Gln	atc Ile	aac Asn 245	aat Asn	gtc Val	agc Ser	gcc Ala	atg Met 250	ctg Leu	gtc Val	ctc Leu	gcc Ala	agg Arg 255	cca Pro	768	
gtg Val	acg Thr	gga Gly	ccc Pro 260	cgg Arg	gag Glu	tac Tyr	gtg Val	ctg Leu 265	gac Asp	ctg Leu	gag Glu	atg Met	gtc Val 270	acc Thr	atg Met	816	
aat Asn	tcc Ser	ctt Leu 275	atg Met	agc Ser	tac Tyr	cgg Arg	gcc Ala 280	agc Ser	tct Ser	gta Val	ctg Leu	aga Arg 285	ctc Leu	acg Thr	gtc Val	864	
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gcccttccc cttcccatag cttaagcagc cccgggggcc tagggatgac cgttctgctt																975	
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<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

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Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

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Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
 195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
 210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

Phe Val Gly Ala Tyr Thr Phe  
 290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 3'

<400> 11

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39

<210> 12

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<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' MCS oligonucleotide

<400> 12  
gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' MCS oligonucleotide

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37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' mMBP1

<400> 14  
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22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

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<400> 15  
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Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu 15

ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc 153  
Leu Leu Leu Gly Ala 25 Ser Pro Gln Asp 30 Glu Glu Pro Asp Ser 35

tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac 201  
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp 45 Asp Ala Asp Ser Gln His 50

tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt 249  
Cys Arg Asp Val 55 Asn Glu Cys Leu Thr 60 Ile Pro Glu Ala Cys Lys Gly 65

gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc 297  
Glu Met 70 Cys Ile Asn His Tyr 75 Gly Gly Tyr Leu Cys Leu Pro Arg 80

tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca 345  
Ser Ala Ala Val Ile Ser Asp 90 Leu His Gly Glu Gly 95 Pro Pro Pro Pro 100

gcg gcc cat gct caa caa cca aac cct tgc ccg gag ggc tac gag cct 393  
Ala Ala His Ala Gln 105 Pro Asn Pro Cys 110 Gln Gly Tyr Glu Pro 115

gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg 441  
Asp Glu Gln Glu Ser 120 Cys Val Asp Val 125 Glu Glu Cys Thr Gln Ala Leu 130

cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac 489  
His Asp Cys Arg Pro Ser Gln Asp Cys 140 His Asn Leu Pro Gly 145 Ser Tyr 150

cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg 537  
Gln Cys Thr 150 Cys Pro Asp Gly Tyr 155 Arg Lys Ile Gly 160 Glu Cys Val 165

gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac 585  
Asp Ile Asp Glu Cys Arg Tyr 170 Arg Tyr Cys Gln His 175 Arg Cys Val Asn 180

ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga 633  
Leu Pro Gly Ser Phe Arg 185 Cys Gln Cys Glu Pro 190 Gly Phe Gln Leu Gly 195

cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc 681  
Pro Asn Asn Arg Ser 200 Cys Val Asp Val 205 Asn Glu Cys Asp Met Gly Ala 210

cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc thr ttc ctg tgt cgc 729  
Pro Cys Glu 215 Arg Cys Phe Asn Ser 220 Tyr Gly Thr Phe Leu Cys Arg 225



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Cys	Asn	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	Cys	Asp				
		230					235					240						
atc	gat	gag	tgc	ggc	tac	tcc	agt	tac	ctc	tgc	cag	tac	cgc	tgt	gtc		825	
Ile	Asp	Glu	Cys	Gly	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val			
	245					250					255							
aac	gag	cca	ggc	cga	ttc	tcc	tgt	cac	tgc	cca	caa	ggc	tac	cag	ctg		873	
Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu			
	260				265					270					275			
ctg	gct	aca	agg	ctc	tgc	caa	gat	att	gac	gag	tgt	gaa	aca	ggt	gca		921	
Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Thr	Gly	Ala			
				280					285					290				
cac	caa	tgt	tct	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg	ggt	tac		969	
His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr			
			295					300					305					
cgc	tgt	gtg	gac	acc	aac	cgt	tgt	gtg	gag	ccc	tat	gtc	caa	gtg	tca		1017	
Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Val	Gln	Val	Ser			
		310					315					320						
gac	aac	cgc	tgc	ctc	tgc	cct	gcc	tcc	aat	ccc	ctt	tgt	cga	gag	cag		1065	
Asp	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln			
	325					330					335							
cct	tca	tcc	att	gtg	cac	cgc	tac	atg	agc	atc	acc	tca	gag	cga	agt		1113	
Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Ser	Ile	Thr	Ser	Glu	Arg	Ser			
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gtg	cct	gct	gac	gtg	ttt	cag	atc	cag	gca	acc	tct	gtc	tac	cct	ggt		1161	
Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly			
				360					365					370				
gcc	tac	aat	gcc	ttt	cag	atc	cgt	tct	gga	aac	aca	cag	ggg	gac	ttc		1209	
Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ser	Gly	Asn	Thr	Gln	Gly	Asp	Phe			
			375					380					385					
tac	att	agg	caa	atc	aac	aat	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	agg		1257	
Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg			
		390					395					400						
cca	gtg	acg	gga	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc		1305	
Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr			
	405					410					415							
atg	aat	tcc	ctt	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	aga	ctc	acg		1353	
Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr			
	420				425					430					435			
gtc	ttt	gtg	gga	gcc	tat	acc	ttc	tgaagaccct	cagggaagg	ccatgtgggg							1407	
Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe											
				440														
gccctctccc	cctcccatag	cttaagcagc	cccgggggcc	tagggatgac	cgcttctgctt												1467	
aaaggaacta	tgatgtgaag	gacaataaag	ggagaaaagaa	ggaaaa													1513	

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<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
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Phe Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

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Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

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<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide 3' hMBP1

<400> 17  
ctccgctccg aggtgatggt c 21

<210> 18  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> oligonucleotide 5' hMBP1

<400> 18  
tgtagctact ccagctacct c 21

<210> 19  
<211> 1122  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Human MBP1 cDNA (partial sequence)

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cttgggatca gcttctctc aggattctga agagcccgac agctacacgg aatgcacaga 180  
tggtctatgag tgggaccag acagccagca ctgccgggat gtcaacgagt gtctgacct 240  
ccctgaggcc tgcaaggggg aatgaagtg catcaaccac tacgggggct acttgtgcct 300  
gccccgctcc gctgccgtca tcaacgacct acacggcgag ggacccccgc caccagtgc 360  
tcccgctcaa caccacaacc cctgcccacc aggtatgag cccgacgatc aggacagctg 420  
tgtggatgtg gacgagtgtg cccaggccct gcacgactgt cgcggcagcc aggactgcca 480  
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gtgtgtggac atagacgagt gccgctaccg ctactgccag caccgctgcg tgaacctgcc 600
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tgttgatgtg aacgagtgtg acatgggggc cccatgcgag cagcgtctgt tcaactccta 720
tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg 780
cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga 840
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ccaagacatt gatgagtgtg agtctggtgc gcaccagtgc tccgaggccc aaacctgtgt 960
caacttccat gggggctacc gctgctgga caccaaccgc tgcgtggagc cctacatcca 1020
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<210> 20

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

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tgtgagtctg gtgcgcacca gtgtcccgag gcccaaacct gtgtcaactt ccatgggggc 180
taccgctgcg tggacaccaa ccgctgcgtg gagccctaca tccaggcttc tgagaaccgc 240
tgtctctgcc cggcctcaa cctctatgt cgagagcagc cttcatccat tgtgcaccgc 300
tacatgacca tcacctcgga gcggagcgtg cccgctgacg tgttcagat ccaggcgacc 360
tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaaact gcagggggac 420
ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctgcgccg gccggtgacg 480
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cggggcagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca 600
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<210> 21

<211> 1480

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<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

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Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag 154  
Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac 202  
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc 250  
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc 298  
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc 346  
Leu Pro Arg Ser Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca gcc 394  
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc 442  
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct 490  
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc 538  
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc 586  
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc 634  
Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac 682

Conseiller.ST25

Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Glu	Cys	Asp		
		195					200					205				
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Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	
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ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	778
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	
225					230					235					240	
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	826
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	
				245					250					255		
cgc	tgc	gtc	aac	gag	cca	ggc	cgT	ttc	tcc	tgc	cac	tgc	cca	cag	ggT	874
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	
			260					265					270			
tac	cag	ctg	ctg	gcc	aca	cgC	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	922
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	
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tct	ggt	gcg	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	970
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	
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ggg	ggc	tac	cgC	tgc	gtg	gac	acc	aac	cgC	tgc	gtg	gag	ccc	tac	atc	1018
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	
305					310					315					320	
cag	gtc	tct	gag	aac	cgC	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	1066
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	
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cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgC	tac	atg	acc	atc	acc	tcg	1114
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	
			340					345					350			
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	1162
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	
	355						360					365				
tac	ccc	ggt	gcc	tac	aat	gcc	ttt	cag	atc	cgT	gct	gga	aac	tcg	cag	1210
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Gly	Asn	Ser	Ser	Gln	
	370					375					380					
ggg	gac	ttt	tac	att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	1258
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	
385					390					395					400	
ctc	gcc	cgg	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	1306
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	
			405						410				415			
atg	gtc	acc	atg	aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	1354
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	
			420					425					430			
agg	ctc	acc	gtc	ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca				1407
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe						
		435				440										

Conseiller.ST25

ccctccctgc agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa 1467  
taaagggaga aag 1480

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

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Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175



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Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Conseiller.ST25

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

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<400> 23
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gcgtcccccac aggatcccgca ggagccggac agctacacgg aatgcacaga tggctatgag    180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct    240
tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgtctc    300
gctgccgtca tcagtgatct ccattggtgaa ggacctccac cgccagcggc ccatgctcaa    360
caaccaaacc cttgcccgca gggctacgag cctgatgaac aggagagctg tgtggatgtg    420
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttcct    480
ggctcctacc agtgacactg ccctgatggt taccgaaaaa ttggaccgca atgtgtggac    540
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cgatgccagt gtgagccagg cttccagttg ggacctaaac accgctcttg tgtggatgtg    660
aatgagtgtg acatgggagc ccatgtgtgag cagcgtgtct tcaactccta tgggaccttc    720
ctgtgtcgtc gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc    780
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<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcaac ggatttggtc gtat

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<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atggtggtga agac

24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-beta-actin oligonucleotide

<400> 26

cggttgccct tggggttcag ggggg

25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-MBP1 oligonucleotide

<400> 27

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21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense MBP1 oligonucleotide

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<400> 28  
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<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>  
<223> sense-beta-actin oligonucleotide

<400> 29  
gtggggcgcc ccaggcacca 20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>  
<223> Human MBP1 C-term fragment

<220>  
<221> CDS  
<222> (1)..(885)

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Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca 192  
Asn Asn Arg Ser Cys Val Asp Phe Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc 240  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att 288  
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac 336

Conseiller.ST25

Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn		
			100					105					110				
gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggt	tac	cag	ctg	ctg		384
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu		
		115					120					125					
gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct	ggt	gcg	cac		432
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Gly	Ser	Gly	Ala	His		
	130					135					140						
cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg	ggc	tac	cgc		480
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg		
	145				150					155					160		
tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag	gtc	tct	gag		528
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu		
				165					170					175			
aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga	gag	cag	cct		576
Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Arg	Gln	Pro		
			180					185					190				
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg		624
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val		
		195					200					205					
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggt	gcc		672
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala		
		210				215					220						
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac		720
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr		
	225				230					235					240		
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	ccg		768
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro		
				245					250					255			
gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc	atg		816
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met		
			260					265					270				
aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	agg	ctc	acc	gtc		864
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val		
		275					280					285					
ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca	ccctccctgc								915
Phe	Val	Gly	Ala	Tyr	Thr	Phe											
		290				295											
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aagaaagtcc	tggtggctga	ggtgggcggg	tcacactgca	ggaagcctca	ggctggggca												1035
gggtggcact	tgggggggca	ggccaaagttc	acctaaatgg	gggtctctat	atgttcaggc												1095
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Conseiller.ST25  
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<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

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 20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
 130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
 165 170 175

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Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe  
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>

<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

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1 5 10 15

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96  
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
20 25 30

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144  
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
35 40 45

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac 192  
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Ile	Asp	Val	Asn	Glu	Cys	Trp	Val	Ser	Pro	Gly	Arg	Cys	Gln	His	
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Thr	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Tyr	Arg	Cys	Ser	Cys	Ala	Ala	Gly
65					70					75					80
ttc	ctt	ttg	gcc	gca	gat	ggc	aaa	cat	tgt	gaa	gat	gtg	aac	gag	tgc
Phe	Leu	Leu	Ala	Ala	Asp	Gly	Lys	His	Cys	Glu	Asp	Val	Asn	Glu	Cys
				85					90					95	
gag	act	cgg	cgc	tgc	agc	cag	gaa	tgt	gcc	aac	atc	tat	ggc	tcc	tat
Glu	Thr	Arg	Arg	Cys	Ser	Gln	Glu	Cys	Ala	Asn	Ile	Tyr	Gly	Ser	Tyr
			100					105					110		
cag	tgc	tac	tgc	cgt	cag	ggc	tac	cag	ctg	gca	gag	gat	ggg	cat	acc
Gln	Cys	Tyr	Cys	Arg	Gln	Gly	Tyr	Gln	Leu	Ala	Glu	Asp	Gly	His	Thr
		115					120					125			
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Cys	Thr	Asp	Ile	Asp	Glu	Cys	Ala	Gln	Gly	Ala	Gly	Ile	Leu	Cys	Thr
	130					135					140				
ttc	cgc	tgt	gtc	aac	gtg	cct	ggg	agc	tac	cag	tgt	gca	tgc	cca	gag
Phe	Arg	Cys	Val	Asn	Val	Pro	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Pro	Glu
145					150					155					160
caa	ggg	tat	aca	atg	atg	gcc	aac	ggg	agg	tcc	tgc	aag	gac	ctg	gat
Gln	Gly	Tyr	Thr	Met	Met	Ala	Asn	Gly	Arg	Ser	Cys	Lys	Asp	Leu	Asp
				165					170					175	
gag	tgt	gca	ctg	ggc	acc	cac	aac	tgc	tct	gag	gct	gag	acc	tgc	cac
Glu	Cys	Ala	Leu	Gly	Thr	His	Asn	Cys	Ser	Glu	Ala	Glu	Thr	Cys	His
			180					185					190		
aat	atc	cag	ggg	agt	ttc	cgc	tgc	cgc	ttt	gat	tgt	cca	ccc	aac	
Asn	Ile	Gln	Gly	Ser	Phe	Arg	Cys	Leu	Arg	Phe	Asp	Cys	Pro	Pro	Asn
		195					200				205				
tat	gtc	cgt	gtc	tca	caa	acg	aag	tgc	gag	cgc	acc	aca	tgc	cag	gat
Ile	Val	Arg	Val	Ser	Gln	Thr	Lys	Cys	Glu	Arg	Thr	Thr	Cys	Gln	Asp
		210				215					220				
atc	acg	gaa	tgt	caa	acc	tca	cca	gct	cgc	atc	cac	tac	cag	ctc	
Ile	Thr	Glu	Cys	Gln	Thr	Ser	Pro	Ala	Arg	Ile	Arg	His	Tyr	Gln	Leu
225					230					235				240	
aat	ttc	cag	aca	ggc	cta	ctg	gta	cct	gca	cat	atc	ttc	cgc	atc	ggc
Asn	Phe	Gln	Thr	Gly	Leu	Leu	Val	Pro	Ala	His	Ile	Phe	Arg	Ile	Gly
				245					250					255	
cct	gct	ccc	ggc	ttt	gct	ggg	gac	acc	atc	tcc	ctg	acc	atc	acg	aag
Pro	Ala	Pro	Ala	Phe	Ala	Gly	Asp	Thr	Ile	Ser	Leu	Thr	Ile	Thr	Lys
			260					265					270		
ggc	aat	gag	gag	ggc	tac	ttc	gtc	aca	cgc	aga	ctc	aat	gcc	tac	act
Gly	Asn	Glu	Glu	Gly	Tyr	Phe	Val	Thr	Arg	Arg	Leu	Asn	Ala	Tyr	Thr
		275					280					285			
ggt	gtg	gta	tcc	ctg	cag	cgg	tct	gtt	ctg	gag	ccg	cgg	gac	ttt	gcc
Gly	Val	Val	Ser	Leu	Gln	Arg	Ser	Val	Leu	Glu	Pro	Arg	Asp	Phe	Ala
		290				295					300				



Conseiller.ST25

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960  
Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca 1009  
Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
325 330

tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tcctaagtg 1069

ctttttgctg tgactctgta acttaactta atcatgctga gctggttggt ctgagtc 1129

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caaggaaaaa tgaaagaaat cattttaaaa ggtttttttt tttgctgttg ttgtttaatg 1609

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<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
65 70 75 80

Conseiller.ST25

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
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Conseiller.ST25  
330

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine N-terminal signal sequence

<400> 34

Ala Val Ala Glu Thr Pro Asp Phe Cys Pro Pro Pro Pro Ser Leu Arg  
1 5 10 15

<210> 35

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human N-terminal signal sequence

<400> 35

Ser Gln Pro Ser Arg Gln Ser Arg Gly Pro Arg Gly Cys Arg Gly Pro  
1 5 10 15

Asn Pro Arg